

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti
Bandman, Olga
- (ii) TITLE OF THE INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
PHOSPHATE COTRANSPORTER
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: US
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0221 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BRAITUT02
 - (B) CLONE: 754412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gln Val Asp Glu Thr Leu Ile Pro Arg Lys Val Pro Ser Leu Cys
 1 5 10 15
 Ser Ala Arg Tyr Gly Ile Ala Leu Val Leu His Phe Cys Asn Phe Thr
 20 25 30
 Thr Ile Ala Gln Asn Val Ile Met Asn Ile Thr Met Val Ala Met Val
 35 40 45
 Asn Ser Thr Ser Pro Gln Ser Gln Leu Asn Asp Ser Ser Glu Val Leu
 50 55 60
 Pro Val Asp Ser Phe Gly Gly Leu Ser Lys Ala Pro Lys Ser Leu Pro
 65 70 75 80
 Ala Lys Ser Ser Ile Leu Gly Gly Gln Phe Ala Ile Trp Glu Arg Trp
 85 90 95
 Gly Pro Pro Gln Glu Arg Ser Arg Leu Cys Ser Ile Ala Leu Ser Gly
 100 105 110
 Met Leu Leu Gly Cys Phe Thr Ala Ile Leu Ile Gly Gly Phe Ile Ser
 115 120 125
 Glu Thr Leu Gly Trp Pro Phe Val Phe Tyr Ile Phe Gly Gly Val Gly
 130 135 140
 Cys Val Cys Cys Leu Leu Trp Phe Val Val Ile Tyr Asp Asp Pro Val
 145 150 155 160
 Ser Tyr Pro Trp Ile Ser Thr Ser Glu Lys Glu Tyr Ile Ile Ser Ser
 165 170 175
 Leu Lys Gln Gln Val Gly Ser Ser Lys Gln Pro Leu Pro Ile Lys Ala
 180 185 190
 Met Leu Arg Ser Leu Pro Ile Trp Ser Ile Cys Leu Gly Cys Phe Ser
 195 200 205
 His Gln Trp Leu Val Ser Thr Met Val Val Tyr Ile Pro Thr Tyr Ile
 210 215 220
 Ser Ser Val Tyr His Val Asn Ile Arg Asp Asn Gly Leu Leu Ser Ala
 225 230 235 240
 Leu Pro Phe Ile Val Ala Trp Val Ile Gly Met Val Gly Tyr Leu
 245 250 255
 Ala Asp Phe Leu Leu Thr Lys Lys Phe Arg Leu Ile Thr Val Arg Lys
 260 265 270
 Ile Ala Thr Ile Leu Gly Ser Leu Pro Ser Ser Ala Leu Ile Val Ser
 275 280 285
 Leu Pro Tyr Leu Asn Ser Gly Tyr Ile Thr Ala Thr Ala Leu Leu Thr
 290 295 300
 Leu Ser Cys Gly Leu Ser Thr Leu Cys Gln Ser Gly Ile Tyr Ile Asn
 305 310 315 320
 Val Leu Asp Ile Ala Pro Arg Tyr Ser Ser Phe Leu Met Gly Ala Ser
 325 330 335
 Arg Gly Phe Ser Ser Ile Ala Pro Val Ile Val Pro Thr Val Ser Gly
 340 345 350
 Phe Leu Leu Ser Gln Asp Pro Glu Phe Gly Trp Arg Asn Val Phe Phe
 355 360 365
 Leu Leu Phe Ala Val Asn Leu Leu Gly Leu Leu Phe Tyr Leu Ile Phe
 370 375 380
 Gly Glu Ala Asp Val Gln Glu Trp Ala Lys Glu Arg Lys Leu Thr Arg
 385 390 395 400
 Leu

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1643 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT02
(B) CLONE: 754412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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AGAACGGTGA  GGATGACCGA  CGTATAGGCG  AGAGCCTAGG  TACGCCATGC  CAGGTCACCG  60
GTCCGGCAAT  TCCCGGGTCG  ACCCACGCGT  CCGCTTGGAG  GGACGCTGGG  TTCAACTTGA  120
AGCCCTTCCA  CAGACATTAA  GTCGGTGAAA  ACCATTCAC  AGGAGAGGAG  AAACACAATG  180
GCCACAAGA  CAGAGTTGAG  TCCCACAGCA  AGGGAGAGCA  AGAACGCACA  AGATATGCAA  240
GTGGATGAGA  CACTGATCCC  CAGGAAAGTT  CCAAGTTTAT  GTTCTGCTCG  CTATGGAATA  300
GCCCTCGTCT  TACATTTCTG  CAATTTTACA  ACGATAGCAC  AAAATGTCAT  CATGAACATC  360
ACCATGGTAG  CCATGGTCAA  CAGCAACAGC  CCTCAATCCC  AGCTCAATGA  TTCTCTGAG  420
GTGCTGCTGT  ITGACTCAT  TGGTGGCCTA  AGTAAAGCCC  CAAAGAGTAT  TCCCTCGAAG  480
TCCTCAATAC  TTGGGGGTGA  GTTTGCAATT  TGGGAAAGGT  GGGGCCCTCC  ACAAGAACGA  540
AGCAGACTCT  GCAGCATTGC  TTTATCAGGA  ATGTTACTGG  GATGCTTTAC  TGCCATCCTC  600
ATAGTGTGGT  TCATTAGTGA  AACCCCTTGG  TGGCCCTTGG  TCTTCTATAT  CTTTGGAGGT  660
GTTGGCTGTG  TCTGCTGCT  TCTCTGGTTT  GTTGTGATT  ATGATGACCC  CGTTTCCTAT  720
CCATGGATAA  GCACCTCAGA  AAAAGAATAC  ATCATATCCT  CCTTGAACAA  ACAGGTCGGG  780
TCTTTAAGC  AGCCCTCTCC  CATCAAAGCT  ATGCTCAGAT  CTCTACCCAT  TTGGTCCATA  840
TGTTTAGGCT  GTTTCAGCCA  TCAATGGTTA  GTTAGCACAA  TGGTTGTATA  CATACCAACT  900
TACATCAGCT  CTGTGTACCA  TGTTAACATC  AGAGACAATG  GACTTCTATC  TGCCCTTCTC  960
TTTATTGTGT  CCTGGTTCAT  AGGCATGGTG  GGAGGCTATC  TGCCAGATTT  TGGCTTAACC  1020
AAAAAGTTTA  GACTCATCAC  TGTGAGGAAA  ATTGCCACAA  TTTTAGGAG  TCCTCCCTCT  1080
TCAGACTCA  TTGTGCTCT  GCCTTACCTC  AATTCGGGCT  ATATCACAGC  AACTGCCTTG  1140
CTGACGCTCT  CTTGCGGATT  AAGCACATGT  GTTCAGTCAG  GGATTTATAT  CAATGTCTTA  1200
GATATTGCTC  CAAGGTATT  CAGTTTCTC  ATGGGAGCAT  CAAGAGGATT  TCGAGCATTA  1260
GCACCTGTCA  TTGTACCCAC  TGTCAGCGGA  TTTCTTCTTA  GTCAGGACCC  TGAGTTTGGG  1320
TCGAGGAATG  TCTTCTTCT  GCTGTTTGCC  GTTAACTGT  TAGGACTACT  CTTCTACCTC  1380
ATATTTGGAG  AAGCAGATGT  CCAAGAATGG  GCTAAAGAGA  GAAAACTCAC  TCGTTTATGA  1440
AGTTATCCCA  CTTGGATGG  AAAAGTCATT  AGGCACCGTA  TTGCATATAA  TAGAAGGCTT  1500
CCGTGATGAA  AATACCAAGT  AAAAGATTTT  TTTTCTCTGT  GGCTCTTTTC  AATTATGAGA  1560
TCAGTTCATT  ATTTTATCA  GACTTTTTTT  TGAGAGAAAT  GTAAGATGAA  TAAAAATCA  1620
AATAAATGA  TAACTAAGA  TGC

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
(B) CLONE: 450532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Met  Gln  Met  Asp  Asn  Arg  Leu  Pro  Pro  Lys  Lys  Val  Pro  Gly  Phe  Cys
1          5          10          15
Ser  Phe  Arg  Tyr  Gly  Leu  Ser  Phe  Leu  Val  His  Cys  Cys  Asn  Val  Ile
          20          25          30
Ile  Thr  Ala  Gln  Arg  Ala  Cys  Leu  Asn  Leu  Thr  Met  Val  Val  Met  Val
          35          40          45

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Thr | Asp | Pro | His | Gly | Leu | Pro | Asn | Thr | Ser | Thr | Lys | Lys | Leu |
| 50 | | | | | | 55 | | | | | 60 | | | | |
| Leu | Asp | Asn | Ile | Lys | Asn | Pro | Met | Tyr | Asn | Trp | Ser | Pro | Asp | Ile | Gln |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Gly | Ile | Ile | Leu | Ser | Ser | Thr | Ser | Tyr | Gly | Val | Ile | Ile | Ile | Gln | Val |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Pro | Val | Gly | Tyr | Phe | Ser | Gly | Ile | Tyr | Ser | Thr | Lys | Lys | Met | Ile | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Phe | Ala | Leu | Cys | Leu | Ser | Ser | Val | Leu | Ser | Leu | Leu | Ile | Pro | Pro | Ala |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Gly | Ile | Gly | Val | Ala | Trp | Val | Val | Val | Cys | Arg | Ala | Val | Gln | Gly |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Ala | Ala | Gln | Gly | Ile | Val | Ala | Thr | Ala | Gln | Phe | Glu | Ile | Tyr | Val | Lys |
| | | 145 | | | 150 | | | | | 155 | | | | | 160 |
| Trp | Ala | Pro | Pro | Leu | Glu | Arg | Gly | Arg | Leu | Thr | Ser | Met | Ser | Thr | Ser |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Gly | Phe | Leu | Leu | Gly | Pro | Phe | Ile | Val | Leu | Leu | Val | Thr | Gly | Val | Ile |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Cys | Glu | Ser | Leu | Gly | Trp | Pro | Met | Val | Phe | Tyr | Ile | Phe | Gly | Ala | Cys |
| | | 195 | | | | 200 | | | | | | 205 | | | |
| Gly | Cys | Ala | Val | Cys | Leu | Leu | Trp | Phe | Val | Leu | Phe | Tyr | Asp | Asp | Pro |
| | | 210 | | | | 215 | | | | | 220 | | | | |
| Lys | Asp | His | Pro | Cys | Ile | Ser | Ile | Ser | Glu | Lys | Glu | Tyr | Ile | Thr | Ser |
| | | 225 | | | 230 | | | | | 235 | | | | | 240 |
| Ser | Leu | Val | Gln | Gln | Val | Ser | Ser | Ser | Arg | Gln | Ser | Leu | Pro | Ile | Lys |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ala | Ile | Leu | Lys | Ser | Leu | Pro | Val | Trp | Ala | Ile | Ser | Ile | Gly | Ser | Phe |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Thr | Phe | Phe | Trp | Ser | His | Asn | Ile | Met | Thr | Leu | Tyr | Thr | Pro | Met | Phe |
| | | 275 | | | | 280 | | | | | | 285 | | | |
| Ile | Asn | Ser | Met | Leu | His | Val | Asn | Ile | Lys | Glu | Asn | Gly | Phe | Leu | Ser |
| | | 290 | | | 295 | | | | | | 300 | | | | |
| Ser | Leu | Pro | Tyr | Leu | Phe | Ala | Trp | Ile | Cys | Gly | Asn | Leu | Ala | Gly | Gln |
| | | 305 | | | 310 | | | | | 315 | | | | 320 | |
| Leu | Ser | Asp | Phe | Phe | Leu | Thr | Arg | Asn | Ile | Leu | Ser | Val | Ile | Ala | Val |
| | | | 325 | | | | | 330 | | | | | 335 | | |
| Arg | Lys | Leu | Phe | Thr | Ala | Ala | Gly | Phe | Leu | Leu | Pro | Ala | Ile | Phe | Gly |
| | | 340 | | | | | 345 | | | | | | 350 | | |
| Val | Cys | Leu | Pro | Tyr | Leu | Ser | Ser | Thr | Phe | Tyr | Ser | Ile | Val | Ile | Phe |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Leu | Ile | Leu | Ala | Gly | Ala | Thr | Gly | Ser | Phe | Cys | Leu | Gly | Gly | Val | Phe |
| | | 370 | | | | 375 | | | | | 380 | | | | |
| Ile | Asn | Gly | Leu | Asp | Ile | Ala | Pro | Arg | Tyr | Phe | Gly | Phe | Ile | Lys | Ala |
| | | 385 | | | 390 | | | | 395 | | | | | 400 | |
| Cys | Ser | Thr | Leu | Thr | Gly | Met | Ile | Gly | Gly | Leu | Ile | Ala | Ser | Thr | Leu |
| | | | 405 | | | | | 410 | | | | | 415 | | |
| Thr | Gly | Leu | Ile | Leu | Lys | Gln | Asp | Pro | Glu | Ser | Ala | Trp | Phe | Lys | Thr |
| | | 420 | | | | | 425 | | | | | | 430 | | |
| Phe | Ile | Leu | Met | Ala | Ala | Ile | Asn | Val | Thr | Gly | Leu | Ile | Phe | Tyr | Leu |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Ile | Val | Ala | Thr | Ala | Glu | Ile | Gln | Asp | Trp | Ala | Lys | Glu | Lys | Gln | His |
| | | 450 | | | | 455 | | | | | 460 | | | | |
| Thr | Arg | Leu | | | | | | | | | | | | | |
| 465 | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 560 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank
 (B) CLONE: 507415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Glu Phe Arg Gln Glu Glu Phe Arg Lys Leu Ala Gly Arg Ala Leu
 1           5           10           15
Gly Arg Leu His Arg Leu Leu Glu Lys Arg Gln Glu Gly Ala Glu Thr
           20           25           30
Leu Glu Leu Ser Ala Asp Gly Arg Pro Val Thr Thr His Thr Arg Asp
 35           40           45
Pro Pro Val Val Asp Cys Thr Cys Phe Gly Leu Pro Arg Arg Tyr Ile
 50           55           60
Ile Ala Ile Met Ser Gly Leu Gly Phe Cys Ile Ser Phe Gly Ile Arg
 65           70           75           80
Cys Asn Leu Gly Val Ala Ile Val Ser Met Val Asn Asn Ser Thr Thr
           85           90           95
His Arg Gly Gly His Val Val Val Gln Lys Ala Gln Phe Asn Trp Asp
 100           105           110
Pro Glu Thr Val Gly Leu Ile His Gly Ser Phe Phe Trp Gly Tyr Ile
 115           120           125
Val Thr Gln Ile Pro Gly Gly Phe Ile Cys Gln Lys Phe Ala Ala Asn
 130           135           140
Arg Val Phe Gly Phe Ala Ile Val Ala Thr Ser Thr Leu Asn Met Leu
 145           150           155           160
Ile Pro Ser Ala Ala Arg Val His Tyr Gly Cys Val Ile Phe Val Arg
           165           170           175
Ile Leu Gln Gly Leu Val Glu Gly Val Thr Tyr Pro Ala Cys His Gly
 180           185           190
Ile Trp Ser Lys Trp Ala Pro Pro Leu Glu Arg Ser Arg Leu Ala Thr
 195           200           205
Thr Ala Phe Cys Gly Ser Tyr Ala Gly Ala Val Val Ala Met Pro Leu
 210           215           220
Ala Gly Val Leu Val Gln Tyr Ser Gly Trp Ser Ser Val Phe Tyr Val
 225           230           235           240
Tyr Gly Ser Phe Gly Ile Phe Trp Tyr Leu Phe Trp Leu Leu Val Ser
           245           250           255
Tyr Glu Ser Pro Ala Leu His Pro Ser Ile Ser Glu Glu Glu Arg Lys
 260           265           270
Tyr Ile Glu Asp Ala Ile Gly Glu Ser Ala Lys Leu Met Asn Pro Val
 275           280           285
Thr Lys Phe Asn Thr Pro Trp Arg Arg Phe Phe Thr Ser Met Pro Val
 290           295           300
Tyr Ala Ile Ile Val Ala Asn Phe Cys Arg Ser Trp Thr Phe Tyr Leu
 305           310           315           320
Leu Leu Ile Ser Gln Pro Ala Tyr Phe Glu Glu Val Phe Gly Phe Glu
           325           330           335
Ile Ser Lys Val Gly Leu Val Ser Ala Leu Pro His Leu Val Met Thr
 340           345           350
Ile Ile Val Pro Ile Gly Gly Gln Ile Ala Asp Phe Leu Arg Ser Arg
 355           360           365
His Ile Met Ser Thr Thr Asn Val Arg Lys Leu Met Asn Cys Gly Gly
 370           375           380
Phe Gly Met Glu Ala Thr Leu Leu Leu Val Val Gly Tyr Ser His Ser

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| | | | | | | |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|-----|
| 385 | | 390 | | 395 | | 400 |
| Lys Gly Val Ala Ile Ser Phe Leu Val Leu Ala Val Gly Phe Ser Gly | | | | | | |
| | 405 | | 410 | | 415 | |
| Phe Ala Ile Ser Gly Phe Asn Val Asn His Leu Asp Ile Ala Pro Arg | | | | | | |
| | 420 | | 425 | | 430 | |
| Tyr Ala Ser Ile Leu Met Gly Ile Ser Asn Gly Val Gly Thr Leu Ser | | | | | | |
| | 435 | | 440 | | 445 | |
| Gly Met Val Cys Pro Ile Ile Val Gly Ala Met Thr Lys His Lys Thr | | | | | | |
| | 450 | | 455 | | 460 | |
| Arg Glu Glu Trp Gln Tyr Val Phe Leu Ile Ala Ser Leu Val His Tyr | | | | | | |
| | 465 | | 470 | | 475 | |
| Gly Gly Val Ile Phe Tyr Gly Val Phe Ala Ser Gly Glu Lys Gln Pro | | | | | | |
| | 485 | | 490 | | 495 | |
| Trp Ala Glu Pro Glu Glu Met Ser Glu Glu Lys Cys Gly Phe Val Gly | | | | | | |
| | 500 | | 505 | | 510 | |
| His Asp Gln Leu Ala Gly Ser Asp Glu Ser Glu Met Glu Asp Glu Val | | | | | | |
| | 515 | | 520 | | 525 | |
| Glu Pro Pro Gly Ala Pro Pro Ala Pro Pro Pro Ser Tyr Gly Ala Thr | | | | | | |
| | 530 | | 535 | | 540 | |
| His Ser Thr Val Gln Pro Pro Arg Pro Pro Pro Pro Val Arg Asp Tyr | | | | | | |
| | 545 | | 550 | | 555 | |
| | | | | | 560 | |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT02
- (B) CLONE: 754412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|-------------------------------------------------------------------|-----|
| ATTTATATCA ATGCTTAGA TATGCTCCA AGGTATTCCA GTTTTCTCAT GGGAGCATCA | 60 |
| AGAGGATTTT CGAGCATAGC ACGTGTCATT GTACCCACTG TCAGTGGATT TCTCTTAGT | 120 |
| CAGGACCCTG AGTTTGGGTG GAGGAATGTC TTCTTCTTGC TGTTTGCCGT TAACCTGTTA | 180 |
| GGACTACTCT TCTACCTCAT ATTTGGAGAA GCAGATGTCC AAGAATGGGC TAAAGAGAGA | 240 |
| AAACTCACTC GTTTATGAAG TTATCCACC TT | 272 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: XLR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTTGATGCTC CCATGAGAAA ACTGG

25

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: XLF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGGATTTTCG AGCATAGCAC CTGTC

25